SEQUENCE LISTING

<110> C. Frank Bennett
      Kenneth Dobie

<120> ANTISENSE MODULATION OF THYROID HORMONE RECEPTOR INTERACTOR 6
EXPRESSION

<130> RTS-0333

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ggcttcaaga ccgctgtctg gagtccccct ttccaggcc atg tcg ggg ccc acc       174
                                            Met Ser Gly Pro Thr
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tgg ctg ccc ccg aag cag ccg gag ccc gcc aga gcc cct cag ggg agg     222
Trp Leu Pro Pro Lys Gln Pro Glu Pro Ala Arg Ala Pro Gln Gly Arg
                10                  15                  20

gcg atc ccc cgc ggc acc ccg ggg cca cca ccg gcc cac gga gca gca     270
Ala Ile Pro Arg Gly Thr Pro Gly Pro Pro Pro Ala His Gly Ala Ala
            25                  30                  35

ctc cag ccc cac ccc agg gtc aat ttt tgc ccc ctt cca tct gag cag     318
Leu Gln Pro His Pro Arg Val Asn Phe Cys Pro Leu Pro Ser Glu Gln
        40                  45                  50

tgt tac cag gcc cca ggg gga ccg gag gat cgg ggg ccg gcg tgg gtg     366
Cys Tyr Gln Ala Pro Gly Gly Pro Glu Asp Arg Gly Pro Ala Trp Val
    55                  60                  65

ggg tcc cat gga gta ctc cag cac acg cag ggg ctc cct gca gac agg     414
Gly Ser His Gly Val Leu Gln His Thr Gln Gly Leu Pro Ala Asp Arg
70                  75                  80                  85

ggg ggc ctt cgc cct gga agc ctg gac gcc gag ata gac ttg ctg agc     462
Gly Gly Leu Arg Pro Gly Ser Leu Asp Ala Glu Ile Asp Leu Leu Ser
                90                  95                  100

acc acg ctg gcc aaa ctg aat ggg ggt cgg ggt cat gcg tca cgg cga     510
```

```
Thr Thr Leu Ala Lys Leu Asn Gly Gly Arg Gly His Ala Ser Arg Arg
            105                 110                 115

cca gac cga cag gca tat gag ccc ccg cca cct cct gcc tac cgc acg      558
Pro Asp Arg Gln Ala Tyr Glu Pro Pro Pro Pro Ala Tyr Arg Thr
            120                 125                 130

ggc tcc ctg aag cca aat cca gcc tcg ccg ctc cca gcg tct ccc tat      606
Gly Ser Leu Lys Pro Asn Pro Ala Ser Pro Leu Pro Ala Ser Pro Tyr
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ggg ggc ccc act cca gcc tct tac act acc gcc agc acc ccg gct ggc      654
Gly Gly Pro Thr Pro Ala Ser Tyr Thr Thr Ala Ser Thr Pro Ala Gly
150                 155                 160                 165

cca gcc ttc ccc gtg caa gtg aag gtg gca cag cca gtg agg ggc tgc      702
Pro Ala Phe Pro Val Gln Val Lys Val Ala Gln Pro Val Arg Gly Cys
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ggc cca ccc agg cgg gga gcc tct cag gct tct ggg ccc ctc ccg ggc      750
Gly Pro Pro Arg Arg Gly Ala Ser Gln Ala Ser Gly Pro Leu Pro Gly
                185                 190                 195

ccc cac ttt cct ctc cca ggc cga ggt gaa gtc tgg ggg cct ggc tat      798
Pro His Phe Pro Leu Pro Gly Arg Gly Glu Val Trp Gly Pro Gly Tyr
                200                 205                 210

agg agc cag aga gag cca ggg cca ggg gcc aaa gag gaa gct gct ggg      846
Arg Ser Gln Arg Glu Pro Gly Pro Gly Ala Lys Glu Glu Ala Ala Gly
            215                 220                 225

gtc tct ggc cct gca gga aga gga aga gga ggc gag cac ggg ccc cag      894
Val Ser Gly Pro Ala Gly Arg Gly Arg Gly Gly Glu His Gly Pro Gln
230                 235                 240                 245

gtg ccc ctg agc cag cct cca gag gat gag ctg gat agg ctg acg aag      942
Val Pro Leu Ser Gln Pro Pro Glu Asp Glu Leu Asp Arg Leu Thr Lys
                250                 255                 260

aag ctg gtt cac gac atg aac cac ccg ccc agc ggg gag tac ttt ggc      990
Lys Leu Val His Asp Met Asn His Pro Pro Ser Gly Glu Tyr Phe Gly
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cag tgt ggt ggc tgc gga gaa gat gtg gtt ggg gat ggg gct ggg gtt     1038
```

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Gln Cys Gly Gly Cys Gly Glu Asp Val Val Gly Asp Gly Ala Gly Val
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```

```
gtg gcc ctt gat cgc gtc ttt cac gtg ggc tgc ttt gta tgt tct aca    1086
Val Ala Leu Asp Arg Val Phe His Val Gly Cys Phe Val Cys Ser Thr
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```

```
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Cys Arg Ala Gln Leu Arg Gly Gln His Phe Tyr Ala Val Glu Arg Arg
310                 315                 320                 325
```

```
gca tat tgc gag ggc tgc tac gtg gcc acc ctg gag aaa tgt gcc acg    1182
Ala Tyr Cys Glu Gly Cys Tyr Val Ala Thr Leu Glu Lys Cys Ala Thr
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```

```
tgc tcc cag ccc atc ctg gac cgg atc ctg cgg gct atg ggg aag gcc    1230
Cys Ser Gln Pro Ile Leu Asp Arg Ile Leu Arg Ala Met Gly Lys Ala
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```

```
tac cac cct ggc tgc ttc acc tgc gtg gtg tgt cac cgc ggc ctc gac    1278
Tyr His Pro Gly Cys Phe Thr Cys Val Val Cys His Arg Gly Leu Asp
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```

```
ggc atc ccc ttc aca gtg gat gct acg agc cag atc cac tgt att gag    1326
Gly Ile Pro Phe Thr Val Asp Ala Thr Ser Gln Ile His Cys Ile Glu
        375                 380                 385
```

```
gac ttt cac agg aag ttt gcc cca aga tgc tca gtg tgc ggt ggg gcc    1374
Asp Phe His Arg Lys Phe Ala Pro Arg Cys Ser Val Cys Gly Gly Ala
390                 395                 400                 405
```

```
ata atg cct gag cca ggt cag gag gag act gtg aga att gtt gct ctg    1422
Ile Met Pro Glu Pro Gly Gln Glu Glu Thr Val Arg Ile Val Ala Leu
                410                 415                 420
```

```
gat cga agt ttt cac att ggc tgt tac aag tgc gag gag tgt ggg ctg    1470
Asp Arg Ser Phe His Ile Gly Cys Tyr Lys Cys Glu Glu Cys Gly Leu
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```

```
ctg ctc tcc tct gag ggc gag tgt cag ggc tgc tac ccg ctg gat ggg    1518
Leu Leu Ser Ser Glu Gly Glu Cys Gln Gly Cys Tyr Pro Leu Asp Gly
                440                 445                 450
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```
cac atc ttg tgc aag gcc tgc agc gcc tgg cgc atc cag gag ctc tca    1566
```

```
His Ile Leu Cys Lys Ala Cys Ser Ala Trp Arg Ile Gln Glu Leu Ser
     455                 460                 465
```

```
gcc acc gtc acc act gac tgc tga gtcttcctag aagtacctgc tgggttctca   1620
Ala Thr Val Thr Thr Asp Cys
470                 475
```

```
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catgaataaa agaccaaaac actacaggct ggctgagcag tgctggtggg tagctgagag   180

ggaggggtg ggaatggaga gctctgcaga ggggtggaga tcggagcctt cagcctcccg    240

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cccccggaga gccctcccct ctcggcagga gggggctgac tcaggagaa atggcagttt    420

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gagtcccaaa cgaggtgcgg gacggaagag ggggtgaagg ccagaggctc ggggcttcaa   600

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tgctgagcag cacgctggcc gagctgaatg ggggtcgggg tcatgcgtca cggcgaccag 300

accgacaggc atatgagccc ccgccacctc ctgcctaccg cacgggctcc ctgaagccaa 360

atccagcctc gccgctccca gcgtctccct atggggsccc cactccagcc tcttacacta 420

ccgccagcac cccggctggc ccagccttcc ccgtgcaagt gaaggtggca cagccagtga 480

ggggctgcgg ccacccaggc ggggagcctc tcaggcctct gggcccctcc cgggcccccca 540

ctttcctctc ccaggccgag gtgaagtctg ggggcctggc tataggagcc agagagagcc 600

aggccagggg ccaaagagga agctgctggg atctctggcc ctgcaggaag aggaagagga 660

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